Please Amend the claims to as follows, without prejudice to subsequent renewal of the specification in its original form. **Per the requirements of 37 C.F.R. § 1.121, the following claims are to be substituted for the corresponding previously pending claims of the same number(s). A marked up version showing the changes to the claims, is attached herewith. For the Examiner's convenience, a complete claim set of the currently pending claims is also submitted herewith.**

9. (AMENDED). The method of claim 8, wherein the two or more parental character strings display low sequence similarity.

10. (AMENDED). The method of claim 8, further comprising determining a sequence for one or more putative recombinant nucleic acids resulting from in silico recombination of the two or more parental character strings at the cross-over sites, and performing one or more in silico simulation of activity for one or more of the putative recombinant nucleic acids or for a protein encoded by one or more of the putative recombinant nucleic acids.

21. (AMENDED). The method of claim 1, wherein the set of oligonucleotides is provided by synthesizing the oligonucleotides to comprise one or more modified parental character string subsequence, which subsequence comprises one or more of:

a parental character string subsequence modified by one or more replacement of one or more character of the parental character string subsequence with one or more different character;

a parental character string subsequence modified by one or more deletion or insertion of one or more characters of the parental character string subsequence;

a parental character string subsequence modified by inclusion of a degenerate sequence character at one or more randomly or non-randomly selected positions;

a parental character string subsequence modified by inclusion of a character string from a different character string from a second parental character string subsequence at one or more position;

a parental character string subsequence which is biased based upon its frequency in a selected library of nucleic acids; and,

a parental character string subsequence which comprises, or encodes a polypeptide that comprises, one or more sequence motif, which sequence motif is artificially included in the subsequence.

25. (AMENDED). The method of claim 1, wherein the plurality of parental character strings comprises at least two parental character strings, wherein the oligonucleotide set comprises at least one oligonucleotide member comprising a chimeric nucleic acid sequence that comprises a subsequence from each of at least two parental character strings, wherein the subsequences from each parental character string are separated by a crossover point.

26. (AMENDED). The method of claim 25, wherein the crossover point is selected by aligning at least one substring of each of at least two of the parental character strings to display pairwise identity between the substrings, and selecting a point within the aligned sequence as the crossover point.

34. (AMENDED). The method of claim 1, further comprising denaturing the recombinant nucleic acid, and contacting the recombinant nucleic acid with at least one additional nucleic acid produced by cleavage of at least one parental nucleic acid.

35. (AMENDED). The method of claim 1, further comprising denaturing the recombinant nucleic acid, and contacting the recombinant nucleic acid with at least one additional nucleic acid produced by cleavage of a parental nucleic acid, which parental nucleic acid is cleaved by one or more of: chemical cleavage, cleavage with a DNAse, and cleavage with a restriction endonuclease.

36. (AMENDED). The method of claim 1, wherein at least one parental nucleic acid encodes one or more or proteins selected from: EPO, insulin, a peptide hormone, a cytokine, epidermal growth factor, fibroblast growth factor, hepatocyte growth factor, insulin-like growth factor, an interferon, an interleukins, a keratinocyte growth factor, a leukemia inhibitory factor, oncostatin M, PD-ECSF, PDGF, pleiotropin, SCF, c-kit ligand, VEGF, G-CSF, an oncogene product, a tumor suppressor, a steroid hormone receptor, a plant hormone, a disease resistance

gene, an herbicide resistance gene product, a bacterial gene product, a monooxygenase, a protease, a nuclease, and a lipase.

93. (AMENDED). A method of producing recombinant nucleic acids, the method comprising:

providing sequences of two or more parental nucleic acids;

selecting cross-over sites for recombination between the sequences of the two or more parental nucleic acids, thereby defining sequences of one or more recombinant nucleic acids that result from a cross-over between at least two of the sequences of the parental nucleic acids;

selecting a sequence of at least one recombinant nucleic acid *in silico* for one or more expected activity; and,

synthesizing a recombinant nucleic acid corresponding to one or more of the selected recombinant sequence.

95. (AMENDED). The method of claim 94, wherein synthesizing the recombinant nucleic acid comprises providing fragments of two or more of the parental nucleic acids and at least one of corresponding bridge oligonucleotides, hybridizing the fragments and the bridge oligonucleotides and elongating the hybridized fragments with a polymerase or a ligase.

96. (AMENDED). The method of claim 93, wherein the sequences of the two or more parental nucleic acids display low sequence similarity.

97. (AMENDED). The method of claim 93, wherein selecting the sequence of at least one recombinant nucleic acid in silico comprises one or more of:

(i) performing an energy minimization analysis of a protein encoded by the selected recombinant sequence;

(ii) performing a stability analysis of at least one protein encoded by the selected recombinant sequence;

(iii) comparing an energy minimized model of at least one protein encoded by the selected recombinant sequence to an energy minimized model of a protein encoded by one or more of the parental nucleic acids;